PCT10

RAW SEQUENCE LISTING   DATE: 01/22/2002
PATENT APPLICATION: US/10/030,019   TIME: 10:29:45

Input Set : A:\candida1.app.txt
Output Set: N:\CRF3\01182002\J030019.raw

Does Not Comply
Corrected Diskette Needed

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 3 <110> APPLICANT: Contreras, Roland
 4         DeBacker, Marianne
 5         Luyten, Walter
 6         Lanaerts, Isabelle
 7         Nelissen, Bart
 8         Reekmans, Rieka
10 <120> TITLE OF INVENTION: Cell death related drug targets in yeast and fungi
12 <130> FILE REFERENCE: JAN-002-PCT
14 <140> CURRENT APPLICATION NUMBER: US/10/030,019
15 <141> CURRENT FILING DATE: 2001-12-26
17 <150> PRIOR APPLICATION NUMBER: 99870141.1
18 <151> PRIOR FILING DATE: 1999-07-01
20 <160> NUMBER OF SEQ ID NOS: 484
22 <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

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RAW SEQUENCE LISTING   DATE: 01/22/2002
PATENT APPLICATION: US/10/030,019   TIME: 10:29:49

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Output Set: N:\CRF3\01182002\J030019.raw

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Input Set : A:\candida1.app.txt
Output Set: N:\CRF3\01182002\J030019.raw

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     22623         900             905             910
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26026 taacaacaat gccaataagg atgaacgaaa gaatagtcat ggtaacatca aaaactcgga 1500
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                    Output Set: N:\CRF3\01182002\J030019.raw

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26091 ataa                                                            5344
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VERIFICATION SUMMARY   DATE: 01/22/2002
PATENT APPLICATION: **US/10/030,019**   TIME: 10:29:51

Input Set : **A:\candida1.app.txt**
Output Set: **N:\CRF3\01182002\J030019.raw**

```
L:14    M:270 C: Current Application Number differs, Replaced Current Application Number
L:15    M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:21503 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:375
L:22419 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:389
L:22610 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:390
L:26010 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:451
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ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/030, 019_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5[th] amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001